Delaval, Jan



From:

Roark, Jessica

Sent:

Wednesday, October 23, 2002 11:26 AM

To: Subject: Delaval, Jan 09/728,420

Jan,

Please search, including pending, the following from 09/728,420:

SEQ ID NO:12 SEQ ID NO:7.

Please also align:

SEQ ID NO:17 and SEQ ID NO:18 SEQ ID NO:12 and SEQ ID NO:17 SEQ ID NO:12 and SEQ ID NO:13.

If you can do a pileup of all these sequences, with SEQ ID NO:12 as the reference, that would be great. If you can't do a pileup, then pairwise as indicated.

Results on paper please.

Thanks!

Jessica H. Roark

CM1 8A03 Mailbox 9E12 Art Unit 1644 703 605-1209

> Jan Delaval Reference Librarian Biotechnology & Chemical Library CM1 1E07 – 703-308-4498 jan.delaval@uspto.gov

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*

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ALIGNMENTS

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RESULT 1
AAB08725
ID AABC
CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
T-lymphocyte activation; type I transmembrane protein; T cell activation;
T cell proliferation; T-cell mediated disorder.
                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                           02-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                 AAB08725;
                                                                                                                                                                                                                                                                                    AAB08725 standard; Protein; 322
                                                                                 Domain
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                                                                                                                                                                                                                      Amino acid sequence of a murine B7RP1 polypeptide.
         WO200046240-A2
                                                             Domain
                                                                     /note= "signal peptide"
47..322
/note= "mature protein"
47..279
/note= "extracellular domain"
                                        /note= "predicted transmembrane domain"
299..322
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10-AUG-2000.

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Best Local :
                                                                           GL50; antigen; antigen presenting cell; T cell proliferation; graft-versus-host disease; autoimmune disease; allergy; viral acquired immune deficiency syndrome; AIDS; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a B7RP1 (B7 related protein-1) polypeptide. The specification also describes a CRP1 (CD28 related protein-1) polypeptide. The polypeptides are involved in T-lymphocyte activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are predicted to be a type I transmembrane protein. The nucleic acids are useful for regulating T cell activation or proliferation in an animal. The polypeptides are useful for treating, preventing ameliorating or diagnosing a T-cell mediated disorder in an animal. They can also be used to identify test molecules that bind to the polypeptides.
                              Mus musculus.
                                                                                                                                                                                                    Amino acid sequence of a murine GL50-1.
                                                                                                                                                                                                                                                                 11-JUN-2001
                                                                                                                                                                                                                                                                                                                       AAB67711;
                                                                                                                                                                                                                                                                                                                                                                                 AAB67711 standard;
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a murine GL50-1 polypeptides. GL50 molecules are antigens on the surface of antigen presenting cells, which costimulate T cell proliferation and bind to costimulatory receptor ligands on T cells. GL50 modulating agents are used to modulate an immune response in a subject. GL50 polypeptides are used to modulate T cell costimulation, and to reduce the proliferation of a tumour cell. Diseases that can be treated using GL50 molecules are graft-versus-host disease, autoimmune disease, allergies, acquired immune deficiency syndrome (AIDS), and viral infections. The GL50 molecules can be used in vaccines GL50 polypucleotides can be used to locate gene regions associated with genetic disease, in tissue typing, and in forensic identification of a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Fig 1; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding a GL50 polypeptide for modulating immune response and reducing the proliferation of a tumour cell - \,
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               301
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                                                                                                                                                                                                                                                                                                  1 MQLKCPCFVSLGTRQPVWKKLHVSSGFFSGLGLFLLLLSSLCAASAETEVGAMVGSNVVL 60
RTRPHRSYTGPKTVQLELTDHA
                                                           LCCVENVALHQNITSISQAESFTGNNTKNPQETHNNELKVLVPVLAVLAAAAFVSFIIYR 300
                                                                                                                                                                                                                       SCIDPHRRHFNLSGLYVYWQIENPEVSVTYYLPYKSPGINVDSSYKNRGHLSLDSMKQGN 120
                                          LCCVENVALHQNITSISQAESFTGNNTKNPQETHNNELKVLVPVLAVLAAAAFVSFIIYR
                                                                                                      RTYTCMSKNGYPEPNLYWINTTDNSLIDTALQNNTVYLNKLGLYDVISTLRLPWTSRGDV
                                                                                                                  RTYTCMSKNGYPEPNLYWINTTDNSLIDTALQNNTVYLNKLGLYDVISTLRLPWTSRGDV 240
                                                                                                                                                              FSLYLKNVTPQDTQEFTCRVFMNTATELVKILEEVVRLRVAANFSTPVISTSDSSNPGQE 180
                                                                                                                                                                              FSLYLKNVTPQDTQEFTCRVFMNTATELVKILEEVVRLRVAANFSTPVISTSDSSNPGQE 180
                                                                                                                                                                                                                                                                                    MQLKCPCFVSLGTRQPVWKKLHVSSGFFSGLGLFLLLLSSLCAASAETEVGAMVGSNVVL 60
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                                                                                                                                                                                                                                                                                                                                                                                                          322 AA;
                                                                                                                                                                                                                                                                                                                                             100.0%;
ilarity 100.0%;
Conservative
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299..322
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47..279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "intracellular cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "hydrophobic transmembrane
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                                                                                                                                                                                                                                                                                                                                             Score 1687; DB 22;
Pred. No. 2.3e-135;
Wismatches 0;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                     graft-versus-host disease, autoimmune disease, allergies, acquired immune deficiency syndrome (AIDS), and viral infections. The GL50 molecules can be used in vaccines. GL50 polynucleotides can be used to locate gene regions associated with genetic disease, in tissue syping, and in forensic identification of a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a murine GL50-2 polypeptides. GL50 molecules are antigens on the surface of antigen presenting cells, which costinulate T cell proliferation and bind to costinulatory receptor ligands on T cells. GL50 modulating agents are used to modulate an immune response in a subject. GL50 polypeptides are used to modulate T cell costinulation, and to reduce the proliferation of a tumour cell. Diseases that can be treated using GL50 molecules are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GL50; antigen; antigen presenting cell; T cell proliferation; tumour; graft-versus-host disease; autoimmune disease; allergy; viral infection; acquired immune deficiency syndrome; AIDS; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding a GL50 polypeptide for modulating immune response and reducing the proliferation of a tumour cell - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a murine GL50-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB67712 standard; Protein; 347
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                                 181
                                                                 181
                                                                                               121
                                                                                                                               121
241 LCCVENVALHQNITSISQAESFTGNNTKNPQETHNNELKVLVPVLAVLAAAAFVSFIIYR
                                                                                                                                                             61
                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                         Local Similarity
les 319; Conserv
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                                                              RTYTCMSKNGYPEPNLYWINTTDNSLIDTALQNNTVYLNKLGLYDVISTLRLPWTSRGDV 240
                                                                                            FSLYLKNVTPQDTQEFTCRVFMNTATELVKILEEVVRLRVAANFSTPVISTSDSSNPGQE 180
                                                                                                            FSLYLKNVTPQDTQEFTCRVFMNTATELVKILEEVVRLRVAANFSTPVISTSDSSNPGQE 180
                                                                                                                                                             SCIDPHRRHFNLSGLYVYWQIENPEVSVTYYLPYKSPGINVDSSYKNRGHLSLDSMKQGN 120
                                                                                                                                                                            SCIDPHRRHFNLSGLYVYWQIENPEVSVTYYLPYKSPGINVDSSYKNRGHLSLDSMKQGN 120
                                                                                                                                                                                                                                                         MQLKCPCFVSLGTRQPVWKKLHVSSGFFSGLGLFLLLLSSLCAASAETEVGAMVGSNVVL
                              RTYTCMSKNGYPEPNLYWINTTDNSLIDTALQNNTVYLNKLGLYDVISTLRLPWTSHGDV
                                                                                                                                                                                                                         Dunussi-Joannopolulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 2; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                          347
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
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                                                                                                                                                                                                                                                                                                        99.0%;
99.7%;
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                        Score 1670;
Pred. No. 7
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                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                        DB 22;
7.1e-134;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                       Length 347;
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RESULT 4
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                                                                                               QΥ
                                                                                                                                                  Query Match
Best Local
                                                                                                                                   Matches
                                                                                                                                                                                                                                                 that can be treated using GL50 molecules are graft-versus-host disease, autoimmune disease, allergies, acquired immune deficiency syndrome (AIDS), and viral infections. The GL50 molecules can be used in vaccines GL50 polynucleotides can be used to locate gene regions associated with genetic disease, in tissue typing, and in forensic identification of a specific disease, in tissue typing, and in forensic identification of a
                                                                                                                                                                                                                                                                                                                                       which costimulate T cell proliferation and bind to costimulatory receptor ligands on T cells. GL50 modulating agents are used to modulate an immune response in a subject GL50 polypeptides are used to modulate T cell costimulation, and to reduce the proliferation of a tumour cell. Diseases
                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a fusion protein, comprising murine GL50 (mGL50) and murine IgG2a (mIgG2A). The fusion protein is used in the course of the invention. The specification describes GL50 polypeptides. GL50 molecules are antigens on the surface of antigen presenting cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GL50; antigen; antigen presenting cell; T cell proliferation; graft-versus-host disease; autoimmune disease; allergy; viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-2001
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid encoding a GL50 polypeptide for modulating immune response and reducing the proliferation of a tumour cell - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF79942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acquired immune deficiency syndrome; AIDS; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of mGL50-mIgG2am fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB67719 standard; Protein; 489
                                                                                                                                                                                                                                    biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ling V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
 70
                               91 YLPYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNTATELVK 150
                                                                  11
                                                                                                31 LGLFLLLLSSLCAASAETEVGAMVGSNVVLSCIDPHRRHFNLSGLYVYWQIENPEVSVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-244938/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTRPHRSYTGPKTVQLELTD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTRPHRSYTGPKTVQLELTD 320
YLPYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNTATELVK
                                                                  LSLVLALLFP-SMASMETEVGAMVGSNVVLSCIDPHRRHFNLSGLYVYWQIENPEVSVTY
                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunussi-Joannopolulos
                                                                                                                                                                                                     489 AA;
                                                                                                                                                                                                                                      sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig
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                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195pp; English.
                                                                                                                                                  73.1%;
                                                                                                                                  Score 1233.5; DB 23
Pred. No. 1.6e-96;
0; Mismatches 8;
                                                                                                                                                                   DB 22;
                                                                                                                                                                     Length
                                                                                                                                   1;
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AAB87395
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AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87412-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and isclude developing products for the diagnosis or treatment of 'proliferative disorders, cancer, tumours, foetal and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing, treating or ametioraction Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1999;
03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endocrine disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene 2 encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune system disorder; AIDS; autoimmune disease; rheumatoid arthrininammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     foetal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQNNTYYLNKLGLYDVISTLRLPWTSRGDVLCCVENVALHQNITSISQAESFTGNNTKNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QETHNNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 564-565; 607pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Young PE,
Shi Y, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US24008
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99US-0152317.
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Y, Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Florence KA;
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on; wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fiscella M,
R, Duan DR,
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Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO:136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lafleur
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eur DW;
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17-JAN-2001; 2001WO-US01349

02-AUG-2001.

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Antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or menzyme linked communoscreta mentioned above, and communoscreta mentioned above, and communoscreta mentioned above, and communoscreta mentioned above.
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Best Local (
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                                                                                                                                                                      Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal dipulmonary disorder; cardiovascular disorder; renal disorder;
                                                                                     WO200154474-A2
                                                                                                                                                           proliferative
                                                                                                                                                                                                                                                                                10-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                        ABB10504 standard; Protein; 344 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosorbent assay (ELISA). The psecreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 299
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US-08-456-104-4
PCT-US95-02576-23
US-08-456-104-4
PCT-US95-02576-23
US-08-205-697A-21
US-08-205-697A-21
US-08-205-697A-21
US-08-702-525-13
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Matches , 30

75;

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142;

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11;

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                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/L09,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315
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REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: RPI-008
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                  Conservative
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            10.4%; Score 175.5; DB 2; 24.8%; Pred. No. 8.1e-08; tive 51; Mismatches 142;
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                                             Length 329;
                Indels
              35;
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            Gaps
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              11;
                                                             ; MOLECULE TYPE: protein US-08-101-624-2
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                             Query Match
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          Best Local Similarity
                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
CORRESPONDENCE LAHIVE & COCKFIELD
TO STREET, Suite 510
                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 5942607e1 CTLA4/CD28 Ligands
TITLE OF INVENTION: Uses Therefor
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
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                                                                                                  TOPOLOGY:
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83 61 143 115 202 175 251	Query Match Query Match Best Local Similarity 23.8%; Pred. No. 1.9e-06; Matches 70; Conservative 53; Mismatches 137; Indels 34; G Qy 23 VSSGFFSGLGLFLLLLSSLCAASAETEVGAMVGSNVVLSCIDPHRRHFNLSGLYVYWQIE : : :: : : : :	RESULT 1 I46691 CD86 precursor - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 14.Feb-1997 #sequence_revision 14.Feb-1997 #text_ch C;Accession: I46691 R;ISONO, T; SetO, A. Immunogenetics 42, 217-220, 1995 A;Title: Cloning and sequencing of the rabbit gene encoding A;Reference number: 146689; MUID:95369849 A;Accession: I46691 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-330 <ison a;cross-references:="" antigen<="" b7-2="" c;superfamily:="" gb.d49842;="" nid:9755098;="" pidn:baa08642.1="" th=""><th>ALIGNMENTS</th><th>30 111.5 6.6 167 2 S29579 31 111.5 6.6 168 1 PMSSRB 32 111 6.6 583 2 I39428 33 110.5 6.6 588 2 JH0506 34 110.5 6.6 588 2 JH0506 35 109.5 6.5 521 2 JC1508 37 109.5 6.5 521 2 JC1508 37 108 6.4 241 2 S69131 38 108 6.4 241 2 S69131 39 108 6.4 523 2 I50478 40 107.5 6.4 523 2 JH0464 41 106.5 6.3 418 1 A32164 42 106.5 6.3 418 1 A42879 43 106 6.3 1259 2 S36126 44 105.5 6.3 1259 2 S36126 45 105.5 6.3 1694 2 S59065</th></ison>	ALIGNMENTS	30 111.5 6.6 167 2 S29579 31 111.5 6.6 168 1 PMSSRB 32 111 6.6 583 2 I39428 33 110.5 6.6 588 2 JH0506 34 110.5 6.6 588 2 JH0506 35 109.5 6.5 521 2 JC1508 37 109.5 6.5 521 2 JC1508 37 108 6.4 241 2 S69131 38 108 6.4 241 2 S69131 39 108 6.4 523 2 I50478 40 107.5 6.4 523 2 JH0464 41 106.5 6.3 418 1 A32164 42 106.5 6.3 418 1 A42879 43 106 6.3 1259 2 S36126 44 105.5 6.3 1259 2 S36126 45 105.5 6.3 1694 2 S59065
LDSMKQGNFSLYLKNVTPQDTQEFTCRVFM 142	Length 330; Indels 34; Gaps 9; HRRHFNLSGLYVYWQIE 82 : : : : : :	<pre>#text_change 23-Jul-1999 encoding T-cell costimulatory mole A08642.1; PID:g755099</pre>		Ig light chain - r platelet-derived g alcam - human adhesion molecule surface glycoprote myelin/oligodendro biliary glycoprote Ig heavy chain (DO neurolin - goldfis biliary glycoprote DM-GRASP precursor B-CAM protein - hu advanced glycosyla neural cell adhesi Ig light chain - r sialoadhesin - mou

RESULT 2
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CD80 precursor - rabbit
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C:Species: Oryctolagus cuniculus (domestic rabbit)
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Immunogenetics 42, 217-220, 1995
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mrNA
A;Residues: 1-299 < ISO>
A;Cross-references: GB:D49843; NID:g755096; PIDN:BAA08643.1; PID:g755097
C;Superfamily: B-lymphocyte restricted antigen B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Homo sapiens (man)
Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change;
Accession: JC7604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comment: This CD86 variant expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: cd86deltaTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ywords: immune response
                                                      264
          229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 KILEEVVRLRVAANFSTPVISTSDSSNPGQERTYTCMSKNGYPEPNLYW-----IN
                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
GTNTMEREESEQTKKREKIHIPERSDEAQRVFKS
                                                                GNNTKNPQETHNNEL - - KVLVPVLAVLAAAAFVS
                                                                                                                                                                                                                                                                                              KILEEVVRLRVAANFSTPVISTSDSSNPGQERTYTCMSKNGYPEP-NLYWINTTDNSLI- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                            YYLPYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNTATELV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLGLFLLLLSSLCAASAETEVGAMVGSNVVLSCIDPHRRHFNLSGLYVYWQIENPEVSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFTGNNTKNPQETHNNELK--VLVPVLAVLAAAAFVSFII----YRRTRPHRSYTG
                                                                                                                          YDGIMQKSQD--NVTELYDVSISLSVSFPDVTSNMTIFCILET-----DKTRLLSSPFSI 228
                                                                                                                                                                                                                                                            RIHQMNSELSVLANFSQPEIVPISNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSTIE 175
                                                                                                                                                                                                                                                                                                                                                                                              VYLG-KEKFDSVHSKYMGRTSFDSDS-----WTLRLHNLQIKDKGLYQCIIHHKKPTGMI 115
                                                                                                                                                                                           -DTALQNNTVYLNKLGLYDVISTLRLPW----TSRGDVLCCVENVALHQNITSISQAESFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLSNILFVMAFILSGAAPLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENLVLNE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PW----SKPKQEPPIDQLPFWVIIPVSGALVLTAVVLYCLACRHVARWKRTRRNEETVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTVDQDLDTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTDNSLIDTALQNNTVYLNKLGLYDVISTLRLPWTSRGDVLCCVENVALHQNITSISQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REHLTSVTLSIRADFPVPSITDIGHPDPNVKR-IRCSASGGFPEPRLAWMEDGEELNAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLLSSLCAASAETEVGAMVGSNVVLSC----IDPHRRHFNLSGLYVYWQIENPEVSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYLPYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNTATELV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLALAGLHFSSGISQVTKSVKEMAALSCDYNISID-----ELARMRIYWQKDQQMV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LYSVSSELDFNVTNNHSIVCLIKYGEL----SVSQIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 176.5; DB 2;
Pred. No. 5.6e-06;
4; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human
                                                                295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.7e-06;
   262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonnefoy, J.Y.; Delneste,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human CD86 mRNA
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RESULT
I49522
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A;Title: Cloning of B7-2: a CTLA-4 counter-receptor A;Reference number: A48754; MUID:94053735
A;Accession: A48754
                                                                                                                     Qy
                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:433597;
A;Map position: 3q13.3-3q21
C:Superfamily: B7-2 antigen
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision
C;Accession: A48754; S39055
                                                                                                                                                             Вþ
                                                                                                                                                                                                                                           Вb
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A; Residues: 7-329 <AZU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 366, 76-79, 1993
A;Title: B70 antigen is a second ligand for A;Reference number: S39055; MUID:94050123
A;Accession: S39055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-329 <FRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB:CD86; CD28LG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:U04343; NID:g439838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Azuma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:L25259; NID:g416368; PIDN:AAA58389.1; PIA;Note: it is uncertain whether Met-1 or Met-7 is the initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate names: B70 glycoprotein; CD86 antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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les 75; Conser
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                                                                                 ERE
                                                                                                                                                                                                     GNNTKNPQETHNNELKVLVPVLAVLAAAAFVSFIIY-----RRTRPHRSY-TGPKTV 314
                                                                                                                                                                                                                                                                                                                                                      KILEEVVRLRVAANFSTPVISTSDSSNPGQERTYTCMSKNGYPEP-NLYWINTTDNSLI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLGLFLLLLSSLCAASAETEVGAMVGSNVVLSCIDPHRRHFNLSGLYVYWQIENPEVSVT 89
                                                                                                                                                             --ELEDPQPPPDH-----IPWITAVLPTVIICVMVFCLILWKWKKKKRPRNSYKCGTNTM
                                                                                                                                                                                                                                             YDGIMQKSQD--NVTELYDVSISLSVSFPDVTSNMTIFCILET----DKTRLLSSPFSI-
                                                                                                                                                                                                                                                                                 -DTALQNNTVYLNKLGLYDVISTLRLPW---TSRGDVLCCVENVALHQNITSISQAESFT
                                                                                                                                                                                                                                                                                                                         RIHQMNSELSVLANFSQPEIVPISNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                              YYLPYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNTATELV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENLVLNE
                                                                                                                       317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 175.5;
Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ng, J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTLA-4 counter-receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID: g416369
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gene B7-2 protein - mouse
G:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I49522

Freeman, G.J.; Borriello, F.; Exp. Med. 178, 2185-2192, 19

в7-2,

an

alternative

CTLA4 counter-receptor that costimulates

J.G.; Ng, J.W.;

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:23:41; Search time 9.50164 Seconds (without alignments) 1312.163 Million cell updates/sec

Title: Perfect score: Sequence: US-09-728-420C-7
1687
1 MQLKCPCFVSLGTRQPVWKK.....RPHRSYTGPKTVQLELTDHA 322

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

number of hits satisfying chosen parameters:

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

190 200 200 200 200 200 200 200 200 200 2		Result
111.5 111.5 111.5 111.5 110.5 110.5 109.5 109.5 108 108 108 105.5 105.5 105.5	1687 599.5 184 177 175.5 162 160 151.5 144.5 148.5 128.5 128.5 129.5 119.5	Score
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ALIGNMENTS

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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). Ling V., Dunussi-Joannopolulos K.;	J. Immunol. 166:7300-7308(2001).	e g150-b and human g150	"Differential expression of inducible costimulator-ligand splice	Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F.,	II330E=F@IIpheIdI	hlood lumphorutes	_	munc	et a, tive brocern char	a novel B7-like prote	rd J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,		STRAIN-C3H/HeJ; TISSUE-Fetal thymus;	UENCE FROM N.A. (ISOFORM 1		Immin jtv 11:423-432/1999).	.":	bomologof by 1 and by 0 is induced	20015817; PubMed=10549624;	ıγmus;	SEQUENCE FROM N.A. (ISOFORM 1).	Nacure 402:02/-032(1999).	l co-stimul	C.L., Van G., Mak T.W., Senaldi G.;	S., Shahinian A.,	Chang D., Chiu L., Dai T., Duncan G.,	naga S.K., Whoriskey J.S., Khare S.D., Sarmient	PubMed=10617205;	ymphocytes;	SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.	NCB1Tax_tD=_10090;	a; Rodentia;	etazoa; Chordata; Craniata; Vertebrata; Euteleosto	(Mouse).	H2 OR B7RP1	Procesti	(Rel. 41, Last annotation update)	(Rel. 40, Last	40, Created)	ICOL_MOUSE STANDARD; PRT; 322 AA.	RESULT 1 ICOL_MOUSE

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SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
B-cell activation; Immune response; Glycoprotein;
Immunoglobulin domain; Signal; Transmembrane; Mul
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                              СКВВОНУВ
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
ARE PRODUCED BY ALTERNATIVE SPICING.
ARE PRODUCED BY ALTERNATIVE SPICING.
-!- TISSUES SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
(PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY
FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S
PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
LSOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY
-!- DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOIESIS: IN THE LIVER AT
14 K TOP
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Patent number W00121796, 29-MAR-2001.
-I- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR LOSS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY COSTIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
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SIMILARITY:
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an email to license@isb-sib.ch).
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CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
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                                                                                                                                                                                      TISSUB-Peripheral blood lymphocytes;

MEDLINB-20465019; PubMed-11007762;

Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D.,

Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han
Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;

"Characterization of a new human B7-related protein: B7RP-1 i
ligand to the co-stimulatory protein ICOS.";

Int. Immunol. 12:1439-1447(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICOL_HUMAN STANDARD; PRT; 302 AA.
075144; Q9NRQ1; Q9HD18;
15-JUL_1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-related protein-1) (B7RP-1).
ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
                    MEDLINE=20126021; PubMed=10657606;
Ling V., Wu P.W., Finnerty H.F., Bean K.M.,
Leonard J.P., Hunter S.E., Zollner R., Thoma
Jacobs K.A., Collins M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Dendritic cell;
MEDLINE=20477846; PubMed=11023515;
Wang S. Zhu G. Chapoval A.I., Dong
"Costimulation of T cells by B7-H2, a
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                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2). TISSUE=Leukocyte;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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  Jacobs K.A., Collins M.;
'Identification of GL50,
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1),
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322 AA;
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35960 MW;
a novel B7-like protein
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Pred. No. 3.8e-129;
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55CCBA4AD12E47E6 CRC64;
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a B7-like molecule
                                             Thomas J.L., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (B7-like protein G150)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF199028; AAF34739.1;
EMBL; AF289028; AAG01176.1;
EMBL; AF216749; AAK16241.1;
EMBL; AB014553; BAA31028.1;
EMBL; AX100595; CAC36465.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 3.
SMART; SM00409; IG; 1.
SMART; SM00410; IG_like;
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599;
InterPro; IPR003006;
InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Prediction of the coding sequences of unidentified human the complete sequences of 100 new cDNA clones from brain we code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain
                                                                                                TRANSMEM
                                                                                                                       DOMAIN
                                                                                                                                                                      SIGNAL
                                                                                                                                                                                            Alternative
                                                                                                                                                                                                                   Immunoglobulin
                                                                                                                                                                                                                                      B-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98403880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EME European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: Ref.4 sequence differs from that shown in posit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART KINNEY, LIVER, PANCREAS, PLACENIA, SKELETAL MUSCLE, BORN KINNEY, LIVER, VARY PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN LYMPH NODES, LEUKOCYTES AND SPLEEN.

INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY TREATMENT WITH TNY-ALPHA IN PERIPHERAL BLOOD B-CELLS AND MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOKINE SECRETION: INDUCES ALSO B-CELL PROLIFERATION AND DIFFERENTIATION INTO PLASMA CELLS. COULDAY AN IMPORTANT ROLE MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY COSTIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).

SUBCELLULAR LOCATION: Type I membrane protecin (By similarity).

ALITERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        onward for an unknown reason.
                                                                                                                                                                                                                                                                                                                                                                                                             605717; -
                                                                                                                                                                                                                                 activation; Immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.-I., Nagase
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164:1653-1657(2000).
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Ig_MHC.
Ig_like.
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

POTENTIAL.
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                                                                                                                    ICOS LIGAND.
EXTRACELLULAR
                                                                                                                                                                                                                Transmembrane;
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             This
                                    CELLS WITHIN 24 HOURS AFTER ACTIVATION.
-:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-:- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-:- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                B lymphocyte
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995
01-MAR-2002
                                                                                                Immunogenetics 42:217-220(1995).

-i- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL-
-i- FUNCTION: RECEPTOR INVOLVED AND INTERLEUKIN 2 PRODUCTION, BY
FOR T LYMPHOCYTE PROLLIERATION AND INTERLEUKIN 2 PRODUCTION, BY
BINDING CD28 OR CTLA-4. MAY PLAY A CRITTCAL ROLE IN THE EARLY
EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
SUCH AS DECIDING BESWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
                                                                                                                                                                                                                   STRAIN=B/J X CHBB:HM;
MEDLINE=95369849; Pub
                                                                                                                                                                                                                                                                                                           Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                   P42071;
                                                                                                                                                                               "Cloning and sequencing of costimulatory molecules.";
                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                    NCBI_TaxID=9986
                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995
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SWISS-PROT entry
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(Rel. 32, Last sequence up
(Rel. 41, Last annotation
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 Institute
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46.2%;
is copyright. stitute of Bio
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  outstation
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Best Local
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P42070;
01-NOV-1995
01-NOV-1995
01-MAR-2002
T lymphocyte
SEQUENCE FROM N.A
                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                           RABIT
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DISULFID
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                                                                               lymphocyte
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                       cuniculus (Rabbit)
Metazoa; Chordata;
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                               Lagomorpha; Leporidae;
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23.8%; Pi
tive 53;
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                              (Rabbit).
hordata; Craniata; Vertebrata; Euteleostomi;
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CYTOPLASMIC (POTIG-LIKE V-TYPE DOTIG-LIKE C2-TYPE DOTIG-LIKE C2-TYPE)
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InterPro; IPR003600; Ig_like.
Pfam; PP00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISODO T. Seto A.;
ISODO T. Seto A.;
ISODO T. Seto A.;
"Cloning and sequencing of the rabbit gene encoding T-cell
costimulatory molecules.";
Immunogenetics 42:217-220(1995).
ITMUNOGENETICS 42:217-220(1995).
ILMUNOGENETICS ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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InterPro; IPR003006; Ig_MHC.
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MEDLINE=95369849; Pub
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SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
      PW---
                                         SFTGNNTKNPQETHNNELK--VLVPVLAVLAAAAFVSFII-----YRRTRPHRSYTG
                                                                                                                                 TTDNSLIDTALQNNTVYLNKLGLYDVISTLRLPWTSRGDVLCCVENVALHQNITSISQAE
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SKPKQEPPIDQLPFWVIIPVSGALVLTAVVLYCLACRHVARWKRTRRNEETVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 177;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYMPHOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATION P
                                                                                                                                                                                                                                                                                                                                                                                                                                                     120;
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(POTENTIAL).
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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          number of hits satisfying chosen parameters:
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          365.5
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Gapop 10.0 , Gapext 0.5
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1687
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sp_plant:*
sp_rodent:*
sp_virus:*
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sp_unclassified:*
sp_rvirus:*
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064381 mus musculu
Q9bdm9 macaca neme
061238 mus musculu
002838 sus scrofa
Q99133 bos taurus
Q9btf1 canis famil
Q9bdm4 macaca mula
Q9xxx6 felis silve
Q99m27 felis silve
Q95116 felis silve
Q46405 bos taurus
                                                                                                                                                                                                                     042404 gallus gall

Q9bxrl homo sapien

Q9ttf2 canis famil

Q91yv7 mus musculu

035531 rattus norv
                                                                                                                                                                                                                                                                                                                                                Description
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45	44	43	42	41	40	39	38	37	36	<u>υ</u>	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
142.5	142.5	142.5	142.5	142.5	144.5	144.5	146	146	47	147.5	148	148	150	151.5	155	158	158	158.5	160	164	165	165	167.5	169	169	69	169.5	172	
8.4	8.4	8.4			8.6									9.0		9.4		9.4	٠					0		0	10.0	0	
359	357	334	319	290	235	235	289	288	584	306	297	288	149	526	321	304	288	290	524	321	290	288	323	292	292	323	275	321	
4	4	4	4	1	σ	σ	σ	σ	4	11	σ							11						0	σ	σ	σ	11	
P78410	015338	Q9BU81	000477	Q9EP73	Q9N0T0	Q9TQS8	Q28347	Q9BDN6	000478	Q9R1Z9	Q9BE99	Q9TT70	Q62810	Q9н458	055202	Q9TQX1	077684	Q62680	Q921K7	Q6262 4	Q9NZQ7	Q28499	Q9BDM2	002758	Q9GMZ8	Q9BDB8	Q9BDN9	035187	
homo	8 homo	homo	000477 homo sapien	Q9ep73 mus musculu	Q9n0t0 canis famil	Q9tqs8 canis famil	Q28347 cercocebus	cerco	homo	Q9r1z9 mus musculu	Q9be99 sus scrofa	(I)	0 ratt	5	O55202 rattus norv	Q9tqx1 canis famil	077684 macaca neme	Q62680 rattus norv	Q921k7 mus musculu	rat	Q9nzq7 homo sapien	Q28499 macaca mula	ercop	002758 felis silve	Q9gmz8 felis silve		Q9bdn9 papio anubi	O35187 rattus norv	

ALIGNMENTS

QY 86 VSVTYYLPYKSPGINVD-SSYKNRG	Qy 30 GIGLFILLLSSLCAASAETEVGAMV	Query Match 21.7%; Score 365.5; DB 13; Lengtl Best Local Similarity 35.6%; Pred. No. 1.7e-23; Matches 106; Conservative 47; Mismatches 122; Indels	DR SMART; SM00410; IG_like; 1. SQ SEQUENCE 296 AA; 33155 MW;	DR Pfam; PF00047; ig; 2. DR SMART; SM00409; IG; 1.	DR InterPro; IPR003006; Iq_MHC.	DR InterPro: IPR003599; Ig.	DR EMBL; Y08823; CAA70058.1;			OX NCBI TaxID=9031:			CD80-LIKE PROTEIN.	01-DEC-2001 (TrEMBLrel, 19,	DT 01-JAN-1998 (TEMBLICE: 05, CI	042404;	042404 PRELIMINARY;	RESULT 1 042404
VSVTYYLPYKSPGINVD-SSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNT 144	GIGLFILLLSSLCAASAETEVGAMVGSNVVLSCIDPHRRHFNLSGLYVYWQIENPE 85	Score 365.5; DB 13; Length 296; Pred. No. 1.7e-23; ; Mismatches 122; Indels 23; Gaps 10;	061572FEB238CC76 CRC64;				MBL/GenBank/DDBO dacabases.				Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Last annotation update)	Last segmence undate)	100+10d)	PRT; 296 AA.	

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RESULT
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Best Local S
tches 86
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01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
COSTIMULATORY MOLECULE.
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
SMART; SM00410; IG_like; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                               Immunoglobulin
SEQUENCE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                            production." Nat. Immun.
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                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                               HG--
                                                                                                                                                                                                   QIENPEVSVTYYLPYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTC- 138
                                                                                                                                                                                                                                                         LHVSSGFFSGLG-LFLLLLSSLCAASAETEVGAMVGSNVVLSCIDPHRRHFNLSGLYVYW
                                                                   TSISQAESFTGNNTKNPQETHNNELKVLVPVLAVLAAAAFV
                                                                                            AEVFWQDGQGVPL-
                                                                                                                 PNLYWINTTONSLIDTALQNNTVYLNKLGLYDVISTLRLPWTSRGDVLCCVENVALHQNI 253
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                                                                                                                                                      ---RVEMNTATELVKILEEVVRLRVAANFSTPVISTSDSSN--PGQERTYTCMSKNGYPE
                                                                                                                                                                                      QLTDTKQLVHSF----AEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCF
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AF302102; AAK15438.1; -
Pro; IPR003599; Ig
                                                                                                                                                                                                                                                                                   ; 88
                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  IPR003006;
                                             ·SVTITGQPMTFPPEALWVTVGLSVCLIALLVALAFV
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IPR003600;
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                                                                                                                                                                                                                                                                                                                              domain.
AA; 33791 MW;
                                                                                          -TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDA
                                                                                                                                         -----VSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPE
                                                                                                                                                                                                                                                                                                                                                                                                            Ig.
Ig_c2.
Ig_like.
                                                                                                                                                                                                                                                                               14.6%; Score 246; Di 30.6%; Pred. No. 3.66 tive 42; Mismatches
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17,
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Last annotation updat
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3.6e-13;
hes 123;
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Matches 78
 Matches
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EMBL; AF106820, ...
InterPro; IPR00306; Ig_wn.
InterPro; IPR003596; Ig_v.
IRR03596; IG_W1.
SMART; SM00406; IGv, II.
PROSITE; PS00290; IG_MIC; UNKNOWN 1.
PROSITE; PS00290; IG_MIC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (3
01-MAY-2000 (3
01-JUN-2001 (3
B7-2 PROTEIN.
                                      Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; BC013807; AAH13807.1; -.
SEQUENCE 309 AA; 34714 MW; 61593C49EFCBOCE
                                                                                                                       Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                      Q91YV7;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
CD86 ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20093996; Yang S., Sim G.-K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9TTF2;
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                     Q91YV7
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EMBL; AF106826; AAF17297.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang S., Sim G.-K.;
"New Forms of Dog CD80 and CD86 Transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecules."
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                                                                                                                                                                                                                                                                                                PT --
                                                                                                                                                                                                                                                                                                                     ITSISQAESFTGNNTKNPQETHNNELKVLVPVLAVLAAAAFVSFIIYRRTRPHRSYTGP
                                                                                                                                                                                                                                                                                                                                                           TAL---QNNTYYLNKLGLYDVISTL--RLPWTSRGDVLCCVE------NVALHQN 252
                                                                                                                                                                                                                                                                                                                                                                                             QMNSDLSVLANFSQPEIMVTSNRTENSGIINLTCSSIQGYPEPKEMYFLVKTENSSTKYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFVMTLLLYGAASMKSQ--AYFNKTGELPCHFTNSQNISLDELVVFWQDQDKLVLYELYR
                                                                                                                                                                                                                                                                                                                                              TVMKKSQNNVT----
                                                                                                                                                                                                                                                                                                                                                                                                           EEVVRLRVAANFSTP-VISTSDSSNPGQERTYTCMSKNGYPEP-NLYWINTTDNS--LID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNTATELVKIL
64;
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78; Conserv
            Similarity
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Conservative
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                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Carnivora; Fissipedia; Canidae;
           10.7%;
23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%; score 181; DB 6; 26.1%; Pred. No. 1.5e-07; tive 46; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                              ELYNVSISLSFSVPEASNVSIFCVLQLESMKLPSLPYNIDAHTK 239
                                                                                                                                                                                                                                                                                               PDGDHILWIAALLVMLVILCGMVF--FLTLRKRK--KKQPGP
53;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                   Last sequence up
           Score 180; DB 11;
Pred. No. 1.7e-07;
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Sciurognathi;
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Mismatches
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thi; Muridae; Murinae; Mus
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                                               CRC64;
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                     Length 309;
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Canis.
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Gaps
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8
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Copyright GenCore version 5.1.3 (c) 1993 - 2002 Compugen Ltd

OM protein - protein search, using sw model

Run on: October 23, 2002, 13:27:51; ; Search time 14.6361 Seconds (without alignments) 1890.790 Million cell updates/sec

Sequence: Title: Perfect score: US-09-728-420C-12 1495 1 MRLGSPGLLFLLFSSLRADT......VAVAIGWVCRDRCLQHSYAG 288

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

number of hits satisfying chosen parameters:

283138

Minimum DB seq Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* pir2:*
pir3:* pir1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	O.	51	4	ω	2	Ľ	No.	Result
108.5	109.5	110	111.5	112	114	114	114	115	115.5	117.5	122	123	124	133.5	133.5	135	139	140.5	142.5	145.5	158	164.5	165.5	171	171.5	179	182	194.5	Score	
7.3	7.3	7.4	7.5	7.5	7.6	7.6	7.6	7.7	7.7	7.9		8.2	8.3			9.0	٠	9.4	9.5	9.7	10.6	11.0	11.1	11.4	11.5	•	12.2	13.0	Match I	
1896	978	299	569	503	702	662	647	739	1256	946	646	333	278	513	509	299	274	321	289	309	330	288	329	526	275	526	309	487	Length I	i
2	2	N	N	Ν	2	N	N	N	N	_	N	2	ш	2	N	Ν	Ν	N	2	2	N	N	\vdash	N	N	N	N	2	BG	
T08851	S16385	S56749	A46462	JC5287	A36319	T16525	B41288	A41288	T03096	A47299	I38049	A31923	TDRTOX	JC5289	JC5288	146690	A47639	I54766	G00031	I49503	146691	A45803	A48754	A37821	JC7604	S70587	I49522	S65133	ID	
Down syndrome cell	macrophage colony-	junctional adhesio	T cell activation	SHP substrate-1 pr		hypothetical prote	vascular cell adhe	vascular cell adhe		ror-related recept		amalgam protein pr	OX-2 membrane glyc	SHP substrate-1 pr	SHP substrate-1 pr	CD80 precursor - r	OX-2 membrane glyc	B-lymphocyte activ	B7 protein - red-c	B-lymphocyte activ	CD86 precursor - r	B-cell-restricted	B7-2 antigen - hum	butyrophilin - bov	CD86 spliced varia	butyrophilin precu	gene B7-2 protein	butyrophilin - mou	Description	

A; Status. Fig. mRNA A; Molecule type: mRNA A; Residues: 1-309 <RES> N: Cross-references: GB:L25606; NID:g432478; PIDN:AAA79770.1; PID:g432479

A; Status: preliminary; translated from GB/EMBL/DDBJ

gene B7-2 protein - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999 C;Accession: 149522

I49522

A; Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell A; Reference number: I49522; MUID:94065585
A; Accession: I49522 R;Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim J. Exp. Med. 178, 2185-2192, 1993

31 32 33 33 34 34 34 34 34 34 34 34 34 34 34	30
107 107 105.5 105.5 105.5 105.5 104.5 104.5 103.5 103.3 103.5	107
7.2 7.2 7.1 7.1 7.1 7.0 7.0 7.0 6.9 6.9 6.8	7.2
1087 1098 584 477 822 588 588 246 1051 1051 1973 973 1880 351	234
222224222244242	Ν
151552 PFMSRB 150419 173631 A105053 JH05054 A47712 A39712 TVMSMD JC2457 TVMSMD JN0581 T18531 S39603 A58532	S14237
platelet-derived g platelet-derived g s-gicerin precurso brain-derived neur brain-derived neur adhesion molecule surface glycoprote myelin/oligodendro kinase-like protei macrophage colony- vascular cell adhe tractin - medicina class I histocompa glial cell membran	Ig kappa chain pre

ALIGNMENTS

butyrophilin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S65133
R;Ishii, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 285-292, 1995
A;Title: Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifica A;Reference number: S65133; MUID:96125722
A;Accession: S65133 Db Qy DЪ Qy Вр Qy В A;Cross-references: GB:S80642; NID:g1246078; PIDN:AAB35893.1; PID:g1246079 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-487 <ISH> Matches Query Match 170 115 144 y Match 13.0%; Score 194.5; DB 2; Local Similarity 31.6%; Pred. No. 5.6e-08; hes 65; Conservative 35; Mismatches 93; 59 25 VRAMVGS-DVELSCACPEGSRFDLNDVYVYWQTSESKTVVTYHIPQNSSLENVDSRYRNR 83 1 VLALVGSDDAELTCGFSPNASSEYMELLWFRQT-RSTAVLLYRDGQEQEGQQM-TEYRGR 58 LRIARTPSVNIGCCIENVLLQQNLTV 228 SAPHSPSQDELTFTCTSINGYPRPNVYWINKTDN-SLLDQALQNDTVFLNMRGLYDVVSV 202 ALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQSLGFQEVLSVEVTLHVAANFSVPVV 143 MMISDSSIKNMSCCIQNILLGQGKEV 195 SMT-VQENGEMELECTSSGWYPEPQVQW--RTGNREMLPST--SDSKKHNEEGLFTVAVS 169 ATLATAGLLDGRATLLIRDVRFSDQGEYRCL-FKDNDDFEE----AAVYLKVAAVGSDPQI 114 DB 2; Length 487; Indels 13; specifically assoc 9;

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JC7604
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$70587
butyrophilin precursor - human
C; Species: Homo sapiens (man)
C; Accession: $70587
R; Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.
Blochim. Biophys. Acta 1306, 1-4, 1996
A; Title: Cloning and sequence analysis of human butyrophilin rev
A; Reference number: $70587; MUID:96201696
A; A; Accession: $70587
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CD86 spliced
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A;Cross-references: EMBL:U39576; NID:g1326082; PIDN:AAC50489.1; PID:g1326083
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-526 < TAY>
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A;Gene: B7-2
C;Superfamily: B7-2 antigen
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                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                        CLLVVVAVAIG 274
                                                                                                                                                                RIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGERDKITENPVSTGEKNAATWSILAVL 263
                                                                                                                                                                                                                                                                                       ALMSPAGMLRGDFSLRLENVTPQDEQKFHCLVLSQSLGFQEVLSVEVTLHVAANFSVPVV 143
                                                                             ILMVLGLLTIG
                                                                                                                                          IIRDTSTKNVSCYIQNLLL--
                                                                                                                                                                                                SM-QVQENGEICLECTSVGWYPEPQVQWRTSKGEKFPSTSESRNP---DEEGLFTVAASV
                                                                                                                                                                                                                               SAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLLDQALQNDTVFLNMRGLYDVVSVL
                                                                                                                                                                                                                                                             ATLVQDGIAKGRVALRIRGVRVSDDGEYTCF-FREDGSYEEAL---VHLKVAALGSDPHI 150
                                                                                                                                                                                                                                                                                                                       ILAVVGEDAELPCRLSPNASAEHLE----LRWFRKKVSPAVLVHRDGREQEAEQMPEYRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILQQTLT---ELSVIANFSEPEIKLAQNVTGNSGINLTCTSKQGHPKPKKMYFLITNSTN 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLAILIFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWQ-DQQKLVLY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EHYLGTEKLDSVNAKYLGRTSFD-----RNNWTLRLHNVQIKDMGSYDCFIQKKPPTGSI 121
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70; Conserv
 variant CD86 deltaTM isoform
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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; Pred. No. 3.2e-07;
61; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 179; DB 2; Pred. No. 1.1e-06;
                                                                                                                                     GQEKKVEISIPASSLPRLTPWIVAVAV
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 526;
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7604
R;Magistrelli, G: Caron, G: Gauchat, J.F.; Jeannin, P: Bonnefoy, J.Y.; Delneste, Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A;Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A;Reference number: JC7604, MUID:21092744; PMID:11162656
A;Accession: JC7604
A;Molecule type: mRNA
A;Residues: 1-275 <MAG>
C;Comment: This CD86 variant expressed by activated human monocytes, is a costimula C;Genetics: This CD86 variant expressed by activated human monocytes is a costimula C;Genetics: Immune response
      밁
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-526 <JAC>
A; Cross-references: GB:M35
C; Keywords: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Jack, L.J.W.; Mather, I.H.
J. Biol. Chem. 265, 14481-14486,
A;Title: Cloning and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991
C:Accession: A37821
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A37821; MUID:90354441
A; Accession: A37821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    butyrophilin - bovine
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                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                    LLFLLFSSLRADT------QEKEVRAMYGSDVELSCACPEGSRFDLNDVYVYW-QTSES
                                                                                                                                                                         LIFILLQLPKLDSAPFDVIGPQEPILAVVGEDAELPCRL--SPNVSAKGMELRWFREKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSQT-----GNDIGERDKI 242
                                         LGFQEVLSVEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSL 179
                                                                                                                             KTVVTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQS 119
                                                                                    PAVFVSREGQEQEGEEM-AEYRGRVSLVEDHIAEGSVAVRIQEVKASDDGEYRCF-FRQD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTNTMEREESEQTKKREKI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LD-----QALQNDTVFLNMRGLYDVVSVLRIA---RTPSVNIGCCIE---NVLLQQNLTV
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24.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1990
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Pred. No. 4.8e-06;
1; Mismatches 135;
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-GEIQLECTSVGWYPEPQVQWRTHRGEEF
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OM protein - protein search, using sw model GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

Run on: October 23, 2002, 13:23:41; Search time 8.49836 Seconds (without alignments) 1312.163 Million cell updates/sec

Title:
Perfect score:
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

US-09-728-420C-12
1495
1 MRLGSPGLLFLLFSSLRADT.....VAVAIGWVCRDRCLQHSYAG 288

Searched: 105224 seqs, 38719550 residues

number of hits satisfying chosen parameters: 105224

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

115 4 4 4 5 5 5 6 5 6 5 6 6 5 6 6 6 6 6 6	Result No.
588.5 203 189 179 165.5 164.5 158 151.5 139 139 139 139 139 139 110 111.5 111.5 111.5 112.3 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.5 113.	Score
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ALIGNMENTS

RP RA RT	R R R	R R R	RA RA	RX	g R	RN	<u> </u>	R R	RA S	RA P	RX.	g R	R	P 7	RT	RA	RA S	R X	1 R	RP	RE RE	PT	RT	RA X	RC	RP	RN	2 6	888) G	EDE	DE :	D D	DT	AC L	RES
SEQUENCE FROM N.A. (ISOFORM 2). Ling V., Dunussi-Joannopolulos K.; "G150 molecules and uses therefor.";	e for large proteins in vitro."; Res. 5:169-176(1998).	"Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new church clones from brain which can		INE=98403880; PubMed=9734811;	SEQUENCE FROM N.A.	4]	J. Immunol. 164:1653-1657(2000).	cification of G	о.ы., мтуа	, Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser	INE=20126021; PubMed=10657606;	SEQUENCE FROM N.A. (ISOFORM 2).		rigand to the co-stimulatory protein icos.";	cterization of a new human B7-related protein: B	noukian R., Whoriskey J.S., Coccia M.A.;	lanev T . Han H	S.K. Zhang M. Pistillo T. Horan T. Khare S.D. Miner K.	blood lymphocytes;		B100d 96:2808-2813(2000).	1	7-H2, a B7-like molecule that binds	15; Dong H., Tamada K., Ni J	י י	SEQUENCE FROM N.A. (ISOFORM 1).	11	la; Frimates;	Chordata; Craniata; Vertebrata; I	, ,	ein-1) (B7RP-1).	ursor (B7 homolog 2)	16-0CT-2001 (Rel. 40, Last sequence update)	. 38, Created)	100E_HOMAN STANDARD; PRT; 302 AA.	

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B
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Best Local Sin
Matches 288;
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InterPro; IPR003006;
InterPro; IPR003600;
InterPro; IPR003600;
Pfam; PF00047; 19; 3.
                                                                                                                                                                               DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent number WO0121796, 29-MAR-2001.

-I FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR TOSS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY COSTIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
                                                                                                                         CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                          Alternative SIGNAL
                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
B-cell activation; Immune r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                     CARBOHYD
                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin domain; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TY CAUTION: Ref: 4 sequence differs from that shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART, KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES, SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN LYMPH NODES, LEUKOCYTES AND SPLEEN.

LYMPH NODES, LEUKOCYTES AND SPLEEN.

INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND MONOCYTES, WHILE IT IS DECREASED IN DENDRIFIC CELLS.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              onward for an unknown reason.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein (By similarity)
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY.
              MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESK 60
MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF199028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF289028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AX100595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF216749;
                                                                  Similarity
                                                                                                           19
19
257
278
37
151
37
158
37
158
70
173
173
173
173
186
225
225
300
300
                                                                                                                                                                                                                                                                                                                                       splicing
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; AAF34739.1; -.; AAG01176.1; -.; AAK16241.1; -.; BAA31628.1; ALT; CAC36465.1; -.
                                                                                                            AA;
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302
256
277
277
302
120
223
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                                                                                                                                     113
216
70
137
173
186
225
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Ig_MHC.
Ig_like.
                                                                                                              33349
                                                                  100.0%;
                                                                                                            ₩;
                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTI

GHV -> ESWALLLLLS (IN ISOFORM 2
                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALT_SEQ.
                                                                  Score
Pred.
                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                           ICOS LIGAND.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                       IG-LIKE V-TYPE DOMAIN.
                                                                                                            647934E21B55E34A CRC64;
                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Multigene family;
                                                     Mismatches
                                                                  1495;
No. 1
                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                  DB 1;
L.4e-122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
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                                                                                                                        (POTENTIAL)
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                                                    Gaps
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60
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RESULT 2
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Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J., Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S., Hui A., McCabe S.M., Scully S., Shahinian A., Shaklee C.L., Van G., Mak T.W., Senaldi G.;

"T-cell co-stimulation through B7RP-1 and ICOS.";
Nature 402:827-832(1999).
                     variants: lymphoid regulation of molecules.";
J. Immura.
                                                                                                                                                                                                                                                              Swallow M.M., "B7h, a novel TNFalpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (Rel. 40, Last sequence update)
ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-related protein-1) (B7RP-1) (LICOS).
ICOSL OR B7H2 OR B7RP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
16-OCT-2001
01-MAR-2002
SEQUENCE FROM
                                                                                    SEQUENCE FROM N.A. (ISOFORM 2).
TISSUE-Peripheral blood lymphoc
MEDLINE-21286479; PubMed-113904
                                                                                                                                  Leonard J.P., Hunter S.E., Zollner R., Jacobs K.A., Collins M.; "Identification of GL50, a novel B7-11% binds to ICOS receptor."; J. Immunol. 164:1653-1657(2000).
                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=C3H/HeJ; TISSUE-Fetal thymus;
MEDLINE=20126021; PubMed=10657606;
Ling V., Wu P.W., Finnerty H.F., Beal
                                                                                                                                                                                                                                                                                             MEDLINE=20015817; PubMed=10549624;
                                                                                                                                                                                                                                                                                                             TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                д9лнл8;
                                                                            Ling V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                           Wu P.W.,
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(Rel. 40,
(Rel. 41,
N.A.
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                                                                                      blood lymphocytes;
PubMed=11390480;
                                                                            Miyashiro
(ISOFORMS 1 AND
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                                                                           J.S.,
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                                            mouse
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                                                                                                                                                                                             Bean K.M.,
                                                                            Marusic
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                                           costimulator-ligand splice gl50-b and human gl50
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                                          g150-b and human
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as J.L., Miyasl
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; Murinae; Mus
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InterPro; IPR003006; I
InterPro; IPR003600; I
Pfam; PF00047; 19; 1.
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-!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR TOURCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL PROLIFERATION AND CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY COSTIMULATING MEMORY TIMEL FUNCTION. DURING PREGNANCY, MAY FUNCTION TO STIMULATING MEMORY TIMEL FUNCTION.
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DISULFID
DISULFID
                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                     TRANSMEM
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SMART; SM00410; IG_like; 1.
B-cell activation; Immune r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
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                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBFAMILY.
SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NONLYMPHOID TISSUES, SUCH AS BRAÍN, HEART, KIDNEY, LIVER, LUNG, SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC CELLS, T-CELLS, DENDRITIC CELLS, AND MACROPHAGES. THE EXPRESSION ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.

DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOIESIS: IN THE YOLK SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.5 DPC
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AX100591;
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IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN
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N-LINKED
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POLY-ALA.
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CYTOPLASMIC
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SEQUENCE FROM N.A.
STRAIN=129; TISSUE-Mammary gland;
STRAIN=07148936; PubMed=8995761;
                                                                                                                                        "Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically associates with a 150-kBa protein of mammary epithelicals and milk fat globule membrane.";
Biochim. Biophys. Acta 1245:285-292(1995).
-!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS.
MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Butyrophilin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel.
15-JUL-1998 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
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Q62556; P97392;
                            <u>;</u>
                                                                                                                                                                                                                                                         TISSUE=Mammary gland; MEDLINE=96125722; PubMed=8541302;
                                                                                                                                                                                                                                                                                      SEQUENCE OF 39-487 FROM N.A.
                                                                                                                                                                                                                                                                                                                                butyrophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BTN1A1 OR BTN.
                                                                                                                                                                                                                                                                                                                 Jog S.L., Komaragiri M.V.S., Mather I.H.;
*Structural organization and mammary-specific expression of
utyrophilin gene.";
yamm. Genome 7:900-905(1996).
                                                                                                                                                                                                                                            Shii T., Aoki N., Noda A., Adachi T.,
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                                        MEMBRANE (BY SIMILARITY).

SUBGUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.

DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF C
PREGNANCY AND IS MAXIMAL DURING LACTATION.
SUBFAMILY.
SIMILARITY:
                          SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TKNPQETHNNEL---KVLVPVLAVLAAAAFVSFIIYRRTRPHRSYTG
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  IMMUNOGLOBULIN-LIKE
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Pfam; PF00622; SPRY; 1.
SMART; SM00406; IGY; 1.
SMART; SM004449; SPRY; 1.
Transmembrane; Glycoprote
   01-NOV-1995 (Rel. 32, Createu, 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 01-MAR-2002 (Rel. 41, Last annotation update) T lymphocyte activation antigen CD86 precursor (Activation T lymphocyte activation antigen CD86) (ETC-1).
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musculus (Mouse)
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IPR003877; SPRY.
IPR003878; SPRY_domain.
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IPR003006; Ig_MHC.
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email to license@isb-sib.ch).
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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EMBL;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                                    [mmunoglobulin
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SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane Drotein.

TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-Type DOMAIN.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
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U39466; AAC52336
                                                          SM00406; IGv;
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                                  domain;
                                  IG_MHC; FALSI
nain; T-cell;
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cell; Glycoprotein;
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T LYMPHOC
LYMPHOCYTE ACTIVATION ANTIGEN CD86
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                                  Signal;
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Maximum Match 100%
Listing first 45 summaries
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   number of hits satisfying chosen parameters:
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Copyright (c) 1993 - 2002 Compugen Ltd.
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O9xsx6 felis silve
O9ymx7 felis silve
O95116 felis silve
O95116 felis silve
O95116 rettus norv
O61238 mus musculu
O61438 humo sapien
O9bdn9 papio anubi
O9tf1 canis famil
O02838 sus scrofa
O92133 bos taurus
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                                                                                                                          042404 gallus gall
29bxrl homo sapien
Q921k7 mus musculu
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	9 mus m		Q9gmz8 felis silve	055202 rattus norv	ratt	000475 homo sapien	Q96av7 homo sapien	Q9nr44 homo sapien	P78410 homo sapien	015338 homo sapien	Q9bu81 homo sapien	homo	Q9nwq6 homo sapien	homo	OMO	Q9jk39 mus musculu	077684 macaca neme	_	3 mus	070356 mus musculu	maca	Q9bq51 homo sapien	home	Q9h730 homo sapien	Q9bdb8 cercocebus	O46535 bos taurus	Q9bdm9 macaca neme	Q9bdm4 macaca mula	Q91yv7 mus musculu

ALIGNMENTS

RESULT 1 042404 Qy 밁 DЪ Ωy Query Match 25.6%; Score 383; DB 13; Best Local Similarity 34.3%; Pred. No. 9.5e-29; Matches 103; Conservative 54; Mismatches 111; 042404 PRELIMINARY; 042404; 01-JAN-1998 (TrEMBLrel. 05, C 01-JAN-1998 (TrEMBLrel. 05, I 01-DEC-2001 (TremBLrel. 19, I InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
SMART; SM00410; IG; 1.
SMART; SM00410; IG; 11.
SMART; SM00410; IG; 11. "Chicken CD28 ligands.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Y08823; CAA70058.1; -. Gallus gallus (Chicken). Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae; CD80-LIKE PROTEIN O'Regan M.N.; STRAIN-WHITE LEGHORN; Gallus. NCBI_TaxID=9031; SEQUENCE FROM N.A 61 57 N SKSCSVVHALISGQDNESQQCSQFKNRTQLLWDKLGDGDFSLLLYNVRQSDEHTYKCVVM 120 SESKTVVTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVL 116 RLGSPGLLFLLESSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQT-----RIGY-GFILLFLHILRAVTALEKIISKPGDNATLSCIYANRG-FDLDSLRVYWQIDGVEG 60 Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasianinae; Created)
Last sequence update)
Last annotation updat 061572FEB238CC76 CRC64; A update) Length 296; Indels 32; Gaps 9;

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RESULT 3
Q921K7
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Q9BXR1
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01-JUN-2001 (TREMBLrel. 17, Las
01-DEC-2001 (TREMBLrel. 19, Las
01-DEC-2001 (TREMBLrel. 19, Las
COSTIMULATORY MOLECULE.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
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MEDLINE-21163383; PubMed-11224528;

Chapoval A.I., Ni J., Lau J.S., Wilcox R.A.,

Dong H., Sica G.L., Zhu G., Tamada K., Chen i
"B7-H3: A costimulatory molecule for T cell
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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SMART; SM00410; IG_like; 2.
Immunoglobulin domain.
SEQUENCE 316 AA; 33791 MW;
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                                                  NPVLQQD-AHGSVT
                                                                       NVLLQQNLTVGSQTGNDIGERDKITENPVSTGEKNAATWSILAVLCLLVVVAVAIGWVC
                                                                                                 YPEAEVFWQDGQGVPLTGNVTTSQ
                                                                                                                                                  GSFTCFVSIRDFG-----SAAVSLQVAAPYSKP--SMTLEPNKDLRPGDTVTITCSSYRG
                                                                                                                                                                 QKFHCLVLSQSLGFQEVLSVEVTLHVAANFSVPVVSAPHSPSQ-----DELTFTCTSING
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102; AAK15438.1;
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Ig_c2.
Ig_like.
Ig_MHC.
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31.1%;
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                                               -ITGQPMTFPPE--ALWVTVGLSVCLIALLVALAFVC
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Last sequence update)
Last annotation updat
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Pred. No. 3.6e-20;
0; Mismatches 111;
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for T cell activation
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-MANEQGLFDVHSVLRVVLGANGTYSCLVR
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RESULT 4
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MEDLINE-21383618; PubMed=11491535;
MEDLINE-21383618; PubMed=A.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Cranıata; ve
Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BDM2;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                          InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig_v.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                              "Cloning, sequencing, and homology analysis Fas/Fas-ligand and co-stimulatory molecules. Immunogenetics 53:315-328(2001).
EMBL, AF344861, AAK37543.1; -.
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                               GLLFLLF--SSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESKTVVT
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Pred. No. 1.3e-
37; Mismatches
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Last annotation update)
BFAMILY 1, MEMBER A1.
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                                                                                        Score 185; DB 6;
Pred. No. 1.4e-09;
9; Mismatches 120;
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1.3e-11;
94;
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SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990_DAT:*
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	18.3 18.3 18.2 18.2 18.1 18.1 17.9		99.7 82.7 81.5 39.4 39.4 39.4 39.4
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Human polypeptide Human B7-H3 polype Human B7-H3 polype Human gene 2 encod Mouse butyrophilin Mouse butyrophilin Guinea pig butyrop Feline CD86 (B7-2) li	B lympho B lympho B lympho polypept membrane gene 2 e polypept polypept polypept	Amino acid sequenc Human pro352 prote Human pro352 (UNQ3 Human BrO polypept Human B7-H3 polype Human gene 2 encod Human am lymphocyte Human amyloid prec Human amyloid prec	immun B7-3 acid acid acid acid acid in encid acid acid

ALIGNMENTS

AAB08727 standard; Protein; 288

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RESULT 1
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ID AABB
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DT 02-J
XX CRPJ
CX T-1y
KW T-1y
KW T-cy
KW T cep
FH Key
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FT Doma CRP1; CD28 related protein-1; B7RP1; B7 related protein-1; T-lymphocyte activation; type I transmembrane protein; T cell activation; T cell proliferation; T-cell mediated disorder. 03-FEB-1999; 08-MAR-1999; 02-JAN-2001 (first entry) AAB08727; 27-JAN-2000; 2000WO-US01871. 10-AUG-2000. WO200046240-A2 Domain Domain Protein Homo sapiens. Amino acid sequence of a human B7RP1 Peptide 99US-0244448. 99US-0264527. /note= "mature protein" 259..274 /note= "signal peptide" 17..288 /note= /note= "predicted transmembrane domain"
275..302 Location/Qualifiers "intracellular domain" polypeptide.

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RESULT 2
AAB0729
ID AAB0
XX AAB0
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                                             Protein
                                                                                                                                                   Homo sapiens
                                                                                                                                                                                          CRP1; CD28 related protein-1; B7RP1; B7 related protein-1; T-1ymphocyte activation; type I transmembrane protein; T crell proliferation; T-cell mediated disorder.
                                                                                                                                                                                                                                                                                                                          02-JAN-2001
                                                                                      Peptide
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N-PSDB; AAA64556.
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                                             /note= "signal peptide" 17..302
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                 hB7-H2; T cell stimulator; immunosuppression; cancer; AIDS; congenital immune deficiency; cellular immune response; inflammatory condition; autoimmune disease; rheumatoid arthritis;
multiple sclerosis; insulin-dependent diabetes mellitus
                                                                                                        Amino acid
                                                                                                                                                 13-NOV-2001
                                                                                                                                                                                                                               AAG67292 standard; Protein; 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-543476/49.
N-PSDB; AAA64557.
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08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                       DQALQNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGERD
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99US-0264527
                                                                                                                                               entry)
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                                                                                                   human hB7-H2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1495; DB 2
Pred. No. 7e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins CRP-1 and B7RP1 are useful diagnosis of T cell mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conditions, and certain congenital immune deficiencies. They may also be employed to increase immune function that has been impaired by the use of radiotherapy or immunosuppressive drugs such as certain chemotherapeutic agents, and therefore are particularly useful when given in conjunction with such drugs or radiotherapy. The hB7-H2 nucleic acid and polypeptide can be used to treat conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a human polypeptide, designated hB7-H2. The hB7-H2 proteins and i wariants are generally useful as immune response-stimulating therapeutics. For example, the polypeptides can be used for treatment of disease conditions characterized by immunosuppression, e.g., cancer, ALDS or ALDS-related complex, other virally or environmentally-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 1A; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                            cell-mediated responses such as those involved in autoimmune diseases (e\cdot g\cdot r) rheumatoid arthritis), multiple sclerosis, or insulin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated DNA encoding a hB7-H2 polypeptide, useful for treating cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2000; 2000US-0186519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2001; 2001WO-US06769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis or M. leprae), or other pathologic
                                                                                                                                                                                                                                                                                                                                                                                                                                             involving cellular immune responses, e.g., inflammatory conditions (such as, for example, those induced by infectious agents including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen
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               DQALQNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGERD 240
                                                                                                                                                                                                                         MRLGSPGLLFLLESSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESK 60
                                                                                      GFQEVLSVEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLL 180
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DQALQNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGERD
                                                                   GFQEVLSVEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLL
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                                                                                                                                                                                                                                                                                                                                              302 AA;
                                                                                                                                                                                                                                                                            Conservative
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27..135
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136..248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH77870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        utoimmune diseases (e.g. rheumatoid arth or insulin-dependent diabetes mellitus)
                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "signal peptide"
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                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                     Score 1495; DB 22;
Pred. No. 7e-130;
Pred. No. 7e-130;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecules can be used in vaccines. GL50 polynucleotides can be used to locate gene regions associated with genetic disease, in tissue typing, and in forensic identification of a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Fig 8; 195pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   graft-versus-host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a GL50 polypeptide for modulating immune response and reducing the proliferation of a tumour cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF79921
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                                                                                                                                                                                                                                                                                     TVVTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQSL 120
        DQALQNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGERD
                                                                                       GFQEVLSVEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLL
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                The present sequence represents a novel human B7-3 protein which acts as a ligand for inducible co-stimulator (ICOS) protein. The B7-3 protein previously referred to as TU-D or KIRAO653 was considered by the 2 groups as being incomplete. The present inventor has determined the sequence to be complete and renamed the sequence as B7-3. Also descrits a soluble form of B7-3 (AAUO0423) which comprises the B7-3 signal sequence and extracellular domain. The extracellular domain is shown bind ICOS which is related to CD28 and expressed on T-cells. B7-3 incomplete.
                                                                                                                                                                                                                   New B7-3 polypeptides useful for modulating inducible co-stimulator protein and for treating ulcers, Crohn's disease, multiple sclerosidiabetes mellitus, infections and allergic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; B7-3; inducible co-stimulator; ICOS; TU-D; KIAA0653; CD28 T-cell; ICOS-mediated activity; IL-10 production; TH2 activity; Helicobacter pylori induced peptic ulcer; Crohn's disease; multiple sclerosis; type I diabetes mellitus; graft rejection; helminth infection; allergic disease.
                                                                                                                                                                                      Claim 1;
     polypeptides
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04-FEB-2000;
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
30-JUN-2000;
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2000US-189874P.
2000US-190076P.
2000US-190123P.
2000US-205515P.
2000US-299467P.
                    2000US-214886P
2000US-215135P
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which interacts with the polypeptide or its fragment. B7-3 polypeptides, fragments, tetramer, an agent with an ability to affect B7-3 activity or a specific binding member are useful for modulating an ICOS-mediated activity of T-cells by modulating IL-10 production and TH2 activity, and for manufacturing a medicament for modulating an ICOS-mediated activity of T-cells. B7-3 polypeptides are useful for development of diagnostic, prophylactic and therapeutic agents for diseases such as Helicobacter prophylactic and therapeutic Trohn's disease, multiple sclerosis, type I diabetes mellitus, graft rejection, helminth infections, and allergic
                                                                                                                                                     ABB10322 standard; Protein; 343
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Human; gene therapy; neural disorder; immune system disorder;
muscular disorder; reproductive disorder; gastrointestinal disorder; proliferative disorder; pulmonary disorder; cardiovascular disorder; 2000US-180628P 2001WO-US01349 2000US-179065P

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                                                The present invention provides human cDNAs, proteins and DNAs. These can be used in the treatment of neural, immu muscular, reproductive, gastrointestinal, pulmonary, car renal and proliferative disorders and inflammation. The is a protein of the invention.
                                                                                                                                                                                                                                                                            Isolated nucleic acid polypeptide is used in condition
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N-PSDB; ABA06544.
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2000US - 235894P.
2000US - 235894P.
2000US - 235894P.
2000US - 235894P.
2000US - 235899P.
2000US - 23599P.
2000US

Sequence

343

AA;

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RRESULT 7
ABB10502
IID ABB11
XX
AC ABB1
XX
DE Huma
XX
Huma
KW Huma
XX
KW Huma
XX
KW Pullr
KW Pullr
KW Prol
XX
KW Pol
XX
W PFO
02-A
PD 02-A
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PF 17-J
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Best Local Similarity
Matches 287; Conserv
    31-JAN-2000

04-FEB-2000

24-FEB-2000

02-MAR-2000

16-MAR-2000

17-MAR-2000

18-APR-2000

07-JUN-2000

07-JUN-2000

07-JUL-2000

07-JUL-2000

07-JUL-2000

11-JUL-2000

11-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferative
                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200154474-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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nilarity 99.7%;
Conservative
    2000US-180628P.
2000US-18464P.
2000US-1846550P.
2000US-189074P.
2000US-199076P.
2000US-199175P.
2000US-205515P.
2000US-205515P.
2000US-21486P.
2000US-215135P.
2000US-215135P.
2000US-217496P.
2000US-22513P.
2000US-22513P.
2000US-225214P.
2000US-225214P.
2000US-225256P.
2000US-225268P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       2001WO-US01349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1494; DB 2
Pred. No. 1e-129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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   14-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
02-OCT-2000
03-OCT-2000
03-NOV-2000
03-NOV-2000
08-NOV-2000
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14-AUG-2000

14-AUG-2000

14-AUG-2000

18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

23-AUG-2000

01-SEP-2000

01-SEP-2000
3000US-22577PP
2000US-225758P
2000US-225758P
2000US-225758P
2000US-225681P
2000US-22579P
2000US-225879P
2000US-225879P
2000US-225879P
2000US-229343P
2000US-229343P
2000US-229343P
2000US-2311414P
2000US-2311414P
2000US-2311414P
2000US-2311414P
2000US-2311414P
2000US-2311414P
2000US-2311414P
2000US-2311414P
2000US-231568P
2000US-231568P
2000US-231568P
2000US-23363P
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2000US-23368P
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2000US-23368P
2000US-23368P
2000US-2341785P
2000US-2341785P
2000US-24477P
2000US-246477P
2000US-246477P
2000US-246477P
2000US-246524P
2000US-246524P
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2000US-246527P
2000US-246526P
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01-DEC-2000

05-DEC-2000

05-DEC-2000

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06-DEC-2000

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08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide is used in condition -
                                                                                                                                                                                                                                                                                                                                                     The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                              Sequence
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                            104
121 GFQEVLSVEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NOV-2000;
                                                                                 61
                                                                                                                           44
                                                                                                                                                                                                                                  Local
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-NOV-2000;
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-NOV-2000;
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                                                                                                                                                 MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESK 60
                                       TVVTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDESLRLENVTPQDEQKFHCLVLSOSL 120
                                                                                                                           MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-476161/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                              345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-249215P.
2000US-249216P.
2000US-249218P.
2000US-249218P.
2000US-249244P.
2000US-249245P.
2000US-249264P.
2000US-249264P.
2000US-249269P.
2000US-24929P.
2000US-24929P.
2000US-24929P.
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2000US-249209P.
2000US-249210P.
2000US-249211P.
2000US-249212P.
2000US-249213P.
2000US-249214P.
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2000US-246532P.
2000US-246609P.
2000US-246610P.
2000US-246611P.
2000US-246613P.
2000US-249207P.
                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-250160P
2000US-250391P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO:
                                                                                                                                                                                                                                                                                              ΑĀ;
                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                              99.9%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              810; 859pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecule encoding an inflammation-associated n preventing, treating or ameliorating a media
                                                                                                                                                                                                          Score 1494; D
Pred. No. 1e-1
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Listing;
                                                                                                                                                                                                                              1494; DB 2
No. 1e-129;
                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                            0,
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                    345;
                                                                                                                                                                                                          0;
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                                                                                                                                                                                                        Gaps
  180
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RESULT 8
AAUI 8065
ID AAUI
XX AAUI
AC AAUI
XX TIMMU
XX IMMU
XX
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18-APR-2000
19-MAY 2000)
07-JUN-2000
30-JUN-2000
30-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
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11-JUL-2000
11-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunoglobulin polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-2001
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CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at fit, wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAU17977-AAU18087 represent immunoglobulin polypeptides of invention. The polypeptides and their associated polynucleotides can used to diagnose a pathological condition or a susceptibility to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-457725/49
N-PSDB; AAS28793.
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                              Local Similarity
                       GFQEVLSVEVTLHVAANFSVPVVSAPHSPSQDELTETCTSINGYPRPNVYWINKTDNSLL 180
                                                                                                                                                                                               MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESK 60
                                                                                                          TVVTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQSL 120
GFQEVLSIEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLL
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                                                                                                                                                                             MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESK 128
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                                                                                                                                                                                                                                                                     Conservative
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2000US-0251988.
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2000US-0249297.
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                                                                                                                                                                                                                                                                                                       AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skin disorder; psoriasis; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder.
                                                                              proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune sy
                                                                                                                                    amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                       treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 564-565; 607pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-1999;
03-SEP-1999;
                              allergies, neurological disorders (e.g., Alzheimer's disease,
                                                      AIDS, autoimmune diseases (e.g., rheumatoid arthritis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing, treating or a Parkinson's diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF91911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB87395;
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Shi Y,
disease), cognitive
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ion; wound healing;
   disorders,
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Olsen HS, Lafleur
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                                                   inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen
eur DW;
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                                                                                    system
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ABB10504
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Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (BIISA). The present sequence represents a human conservation of the invention.
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  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                         Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal dipulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.
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287; Conservative
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2000US-188350P.
2000US-19874P.
2000US-199074P.
2000US-199075P.
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0; Mismatches
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99.7%;

Score 1490; Pred. No. 2

DB 22; No. 2.4e-129; Mismatches

Indels Length

Gaps

0

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240 222

344; 0;

0;

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20-OCT 2000

20-OCT 2000

20-OCT 2000

20-OCT 2000

20-OCT 2000

01-NOV 2000

08-NOV 2000

17-NOV 2000

17-NO
        The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence
                                                                                                                                           Claim 11;
                                                                                                                                                                                                                 Isolated nucleic acid r
polypeptide is used in
                                                                                                                                                                                                                                                                                                                            2001-476161/51
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24-FEB 2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
07-JUL-2000
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14-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2001;
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2000US-0199076
2000US-0199123
2000US-0209467
2000US-0214886
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Protein;

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polypeptide

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2000US-0225268. 2000US-0225270. 2000US-0225447. 2000US-0225757. 2000US-0225758. 2000US-0225759.

2000US-0228924. 2000US-0229287. 2000US-0229343.

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Sequences AAU17977-AAU18087 represent immunoglobulin polypeptides of the CC invention. The polypeptides and their associated polynucleotides can be CC used to diagnose a pathological condition or a susceptibility to a CC pathological condition in a subject by determining the presence or CC absence of a mutation in a DNA sequence or determining the presence or CC amount of expression of the protein. Alternatively the identification of CC a binding partner to a sequence allows determination of changes in CC protein activity. The sequences can be used as research tools for CC receptors or other signal transduction pathway proteins that interact CC with the polypeptides of the invention and can be used to treat, prevent CC or diagnose various types of disorders such as neurological disorders, cardiovascular disorders gastrointestinal disorders, reproductive CC disorders, immune system disorders, renal disorders, muscular disorders, proliferative disorders and cancer.
CC Note: The sequence data for this pattent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
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N-PSDB;
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2000US-02461786
2000US-0246475
2000US-0246475
2000US-02464778

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RESULT 13
AAU00423
ID AAU00
XX AU00
XX AU00
XX 11-MA
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KW T-cell
KW Helic
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KW Helmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; B7-3; inducible co-stimulator; ICOS; TU-D; KIAA0653; CD28; T-cell; ICOS-mediated activity; II-10 production; TH2 activity; Helicobacter pylori induced peptic ulcer; Crohn's disease; multiple sclerosis; type I diabetes mellitus; graft rejection; helminth infection; allergic disease.
                     11-AUG-1999;
                                                                10-AUG-2000; 2000WO-GB03079.
                                                                                                               22-FEB-2001
                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                       WO200112658-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Beta-strand C'
inhibitors of t
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Pred. No. 2.4e-129;
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CC The present sequence represents human B7-3 soluble form protein which CC acts as a ligand for inducible co-stimulator (ICOS) protein. The B7-3 CC soluble form protein comprises the B7-3 signal sequence and CC extracellular domain. The extracellular domain is shown to bind ICOS CC which is related to CD28 and expressed on T-cells. The B7-3 protein CC (AAU00422) previously referred to as TU-D or KIAA0653 was considered by CC the 2 groups as being incomplete. The present inventor has determined CC the sequence to be complete and renamed the sequence as B7-3. B7-3 CC polypeptides or its fragments are useful for identifying a substance CC which interacts with the polypeptide or its fragment. B7-3 polypeptides, CC fragments, tetramer, an agent with an ability to affect B7-3 activity or CC a specific binding member are useful for modulating an ICOS-mediated activity of T-cells by modulating II-10 production and TH2 activity, and CC for manufacturing a medicament for modulating an ICOS-mediated activity of T-cells. B7-3 polypeptides are useful for development of diagnostic, CC prophylactic and therapeutic agents for diseases such as Helicobacter CC prophylactic and therapeutic agents for disease, multiple sclerosis, type Cd disease mellitus, graft rejection, helminth infections, and allergic
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New B7-3 polypeptides useful for modulating inducible co-stimulator protein and for treating ulcers, Crohn's disease, multiple sclerosia diabetes mellitus, infections and allergic diseases
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N-PSDB; AAS00424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS INNOVATIONS LTD.
239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77pp; English.
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Query Match Best Local S Matches 239 181 181 121 121 61 61 1 MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESK DQALQNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGER 239 GFQEVLSVEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLL TVVTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQSL TVVTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQSL MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESK DQALQNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGER GFQEVLSVEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLL al Similarity 239; Conserv Conservative 82.7%; Score 1236; DB 22; 100.0%; Pred. No. 4.4e-106; 0; Mismatches Indels Length 239; 0; Gaps 239 60 60 120 120 0

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RESULT 14
AAB67718
ID AAB67
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AAB67718 standard; Protein; 490

AAB67718;

11-JUN-2001 (first entry)

Amino acid sequence of hGL50-mIgG2am fusion protein

GL50; antigen; antigen presenting cell; T cell proliferation; graft-versus-host disease; autoimmune disease; allergy; viral acquired immune deficiency syndrome; AIDS; vaccine infection

Synthetic

Homo sapiens

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RESULT 15
AAB08725
ID AAB08
XX
AC AAB08
XX
DT 02-JA
XX
DE Amino
XX
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ligands on T cells. GL50 modulating agents are used to modulate an immune response in a subject. GL50 polypeptides are used to modulate T cell costimulation, and to reduce the proliferation of a tumour cell. Diseases that can be treated using GL50 molecules are graft-versus-host disease, autoimmune disease, allergies, acquired immune deficiency syndrome (AIDS), and viral infections. The GL50 molecules can be used in vaccines. GL50 polynucleotides can be used to locate gene regions associated with genetic disease, in tissue typing, and in forensic identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GL50 molecules are antigens on the surface of antigen presenting cells, which costimulate T cell proliferation and bind to costimulatory receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a fusion protein, comprising human GL50 (hGL50) and murine IgG2a (mIgG2A). The fusion protein is used in the course of the invention. The specification describes GL50 polypeptides.
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N-PSDB; AAF79941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 28B; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding a GL50 polypeptide for modulating immune response and reducing the proliferation of a tumour cell - \,
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                Amino acid sequence of a murine
                                                02-JAN-2001
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                                                                                                               AAB08725 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 VLALLFPSMA--SMEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESKTVVTYHI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 LLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESKTVVTYHI 67
                                                                                                                                                                                                                                                         TVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGERDKITENPV 247
                                                                                                                                                                                                                                                                                                                                          VEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLLDQALQND 187
                                                                                                                                                                                              STGEKN
                                                                                                                                                                                                                            STGEKN 253
                                                                                                                                                                                                                                                                                                                           VEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLLDQALQND
                                                                                                                                                                                                                                                                                                                                                                                       PQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQSLGFQEVLS
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237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      490 AA;
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                                               (first entry)
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Pred. No. 5.4e
3; Mismatches
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               B7RP1 polypeptide
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.4e-104;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRP1; CD28 related protein-1; B7RP1; B7 related protein-1; T-lymphocyte activation; type I transmembrane protein; T cell activation; T cell proliferation; T-cell mediated disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 2A; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids encoding in the treatment, prevention
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N-PSDB; AAA64555.
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08-MAR-1999;
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DKITENPVSTGEKNAATWSILAVLCLLVVVAVAIGWVCRDRCLQH-SYAG
                                                                                                 LSVEYTLHVAANFSVPVVSAPHS---PSQDELTFTCTSINGYPRPNVYWINKTDNSLLDQA 183
                                                                                                                                                                  IPONSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLV-LSQSLGFQEV 125
                                                                                                                                                                                              GLFLLLLSSLCAASAETEVGAMVGSNVVLSCIDPHRRHFNLSGLYVYWQIENPEVSVTYY
                         LQNNTVYLNKLGLYDVISTLRLPWTSRGDVLCCVENVALHQNITSISQAESFTGNN----
                                                   LQNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQ----TGNDIGER 239
                                                                                 LEEVVRLRVAANFSTPVISTSDSSNPGQ-ERTYTCMSKNGYPEPNLYWINTTDNSLIDTA
                                                                                                                                         LPYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNTATELVKI
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135; Conserv
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Pred. No. 4.6e-46;
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Db 267 ---TKNPQETHNNEL---KVLVPVLAVLAAAAFVSFIIYRRTRPHRSYTG 310

Search completed: October 23, 2002, 13:29:41 Job time : 26.9672 secs

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Result
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is derived by analysis of the total score distribution.
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      Issued_Patents_AA:*
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US-08-280-75PB-23
US-08-205-697A-21
US-08-205-697A-21
US-08-702-525-21
US-08-702-525-613
US-08-702-525-613
US-08-702-525-613
US-08-702-694-2-2
US-08-101-624-2
US-08-101-624-2
US-08-702-525-23
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13, Appl
13, Appl
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US-08-702-525-19 US-08-403-798-2 US-08-403-253A-2 US-08-403-364-36 US-09-410-384-36 US-09-171-945-131 US-08-630-172-15 US-08-630-172-15 US-08-702-525-2 US-08-702-525-6-2 US-08-702-525-17 US-08-702-525-17 US-08-702-525-17 US-08-703-525-17 US-08-703-525-17 US-08-703-525-17 US-08-703-525-17 US-08-703-525-17 US-08-703-525-17 US-08-703-525-17 US-08-703-525-17 US-08-703-525-17 US-08-17-773-4 US-08-147-772-4

ALIGNMENTS

US-08-456-104-4 RESULT 1

Sequence 4, Application US/08456104
Patent No. 5861310

GENERAL INFORMATION:

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; MOLECULE TYPE: protein US-08-456-104-4
Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                                                                    TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
                                                                                                                                                                                                                 NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109
APPLICATION NUMBER: 19-AUG
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/456,104 FILING DATE: CLASSIFICATION: 424
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                                                                                                                        TOPOLOGY:
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                  12.2%; Score 182; DB 2
23.6%; Pred. No. 3e-10;
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19-AUG-1993
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                                      DB 2;
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                                      Length 309;
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Conservative

61;

Mismatches

117;

Indels

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Gaps

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US-08-479-744A-23
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    Query Match
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                                                                                                                                                         TELEFAX: (617) 227-594 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-479-744A-23
                                                                                                                                                                                                                             ATTIONNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REGISTRATION NUMBER: RPI-004CP3
                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
                                                             MOLECULE TYPE:
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: RF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRENT AFFLECTION NUMBER: US/US/
APPLICATION NUMBER: US/US/
FILING DATE: June 7, 1995
FILING DATE: 435
                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 26-JUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                              (617) 227-5941
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    12.2%;
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    Score 182;
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Length 309;
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RESULT 3
US-08-280-757B-23
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 23.6 Matches 70; Conservative
                                                                                          TELEFAX: (617)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                        FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
MOLECULE TYPE:
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                           FILING DATE: 26-JULY-199;
APPLICATION NUMBER: 08/11
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/1-
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/10.
APPLICATION NUMBER: 08/10.
APPLICATION NUMBER: 08/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COEFFICIENT PC-DOS/MS-DOS
                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                 NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                 TOPOLOGY:
                                                     LENGTH:
                                                                                                                               TELEPHONE:
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Gray, Gary S.
Greenfield, Edward
NVENTION: No. 6130316el CTLA4/CD28 Ligands and
NVENTION: Uses Therefor
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                                                                                                                               (617)
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1; Mismatches 117;
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                                                                                                                     US-08-205-697A-21
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                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Freeman,
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el FORT
TITLE OF INVENTION: and Uses Therefor
TITLE OF INVENTION: 61
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: LL...
OPERATING SYSTEM: PUTL
TORMWARE: ASCII Text
TORMWARE: ASCII Text
                                                                                                                                                                                                                                                                      NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BW3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/205,697A FILING DATE: 02-Mar-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                      MOLECULE TYPE: protein
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                                                        Local
                                                                                                                                                            TOPOLOGY:
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7 GLLFLLFSS--LRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESKTVVT 64
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                                      l Similarity
70; Conserv
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                                                                                                                                                        I: 309 amino acids amino acid 
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sharpe, Arlene H.
Borriello, Francescopaulo
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                                        Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                      12.2%; Score 182; DB 4
23.6%; Pred. No. 3e-10;
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                                    61;
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Pred. No. 3e-10;
                                    Mismatches
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                                                                           DB 4; Length 309;
                                      117;
                                    Indels
                                    48;
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RESULT 5
US-08-702-525-21
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                                                                                                                                                   ; MOLECULE TYPE: protein US-08-702-525-21
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Patent No. 6294660
                                                                                                             Query Match
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                                                                                                                                                                                                                                                                         TELEFAX: (617)227-594 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compa
OPERATING SYSTEM: PC-D
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-Mar-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 --- DNSLLDQALQNDTVFLNMRGLYDVVSVLRIARTPSV---NIGCCIENVLLQQNLTVG
                                                                                                                                                                                                                                                                                                                                                   NAME: Mandragouras, Amy E, REGISTRATION NUMBER: 36,207 REFERENCE/DOCKET NUMBER: BW
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CITY: Boston
                                                                            Local Similarity
les 70; Conserv
                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                LENGTH:
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GLAILIFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWQ-DQQKLVLY 66
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                                                                                                                                                                                                        : 309 amino acids
amino acid
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Borriello, Francescopaolo
Freeman, Gordon
                                                                                                                                                                                                                                                                                           (617)227-5941
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                                                                            Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                               (617)227-7400
                                                                        12.2%; Score 182; DB 4; 1
23.6%; Pred. No. 3e-10;
ative 61; Mismatches 117;
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                                                                                                               DB 4; Length 309
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PCT-US95-02576-21
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PCT-US95-02576-21
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Best Local Similarity
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GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: CYSTEM: PC-DOS/MS-DOS
,122 ILQQTLT---ELSVIANFSEPEIKLAQNVTGNSGINLTCTSKQGHPKPKKMYFLITNSTN 178
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acid
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NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWJ
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OPERATING SYSTEM: PC-D
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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CITY: Boston
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                                     GFQEVLSVEVTLHVAANFSVPVVS-APHSPSQDELTFTCTSINGYPRP-NVYWI--NKT- 175
                                                                                                           YHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLENVTPQDEQKFHCLVLSQ----SL 120
                                                                           EHYLGTEKLDSVNAKYLGRTSFD-----RNNWTLRLHNVQIKDMGSYDCFIQKKPPTGSI 121
                                                                                                                                                    GLAILIFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWQ-DQQKLVLY 66
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60 State Street, suite 510
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(617)227-5941
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                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                              12.2%; Score 182; DB 5; I
23.6%; Pred. No. 3e-10;
tive 61; Mismatches 117;
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APPLICANT: Sharpe, PAPPLICANT: Freeman,
APPLICANT: Freeman,
APPLICANT: Nadler, I
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: BW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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  230
                                        184 EYGDNMQISQD------NVTELFSISNSLSLSFPDGVWHMTVVCVLET----ESMKIS
                                                                                                                        127 ILQQTLT---ELSVIANFSEPEIKLAQNVTGNSGINLTCTSKQGHPKPKKMYFLITNSTN 183
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TYPE: amino acid
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SQTGNDIGERDKITENPVSTGEKNAATWSILAVLCLLVVVAVAIGWVCRDRCLQHS
                                                                                                                                                                 GFQEVLSVEVTLHVAANFSVPVVS-APHSPSQDELTFTCTSINGYPRP-NVYWI--NKT- 175
                                                                                                                                                                                                                                                YHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQ----SL 120
                                                                                                                                                                                                                                                                                           GLAILIFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWQ-DQQKLVLY 71
                                                                               ~--DNSLLDQALQNDTVFLNMRGLYDVVSVLRIARTPSV---NIGCCIENVLLQQNLTVG
                                                                                                                                                                                                         EHYLGTEKLDSVNAKYLGRTSFD-----RNNWTLRLHNVQIKDMGSYDCFIQKKPPTGSI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 3.1e-10;
1; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 314;
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US-08-702-525-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
8-702-525-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/702,55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Freeman, Gordon
APPLICANT: Naddler, Lee
TITLE OF INVENTION: No. 6294660el
TITLE OF INVENTION: Molecules and
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 314 amino acid
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  232
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                     SQTGNDIGERDKITENPVSTGEKNAATWSILAVLCLLVVVAVAIGWVCRDRCLQHS 285
                                                                                                                 ---DNSLLDQALQNDTVFLNMRGLYDVVSVLRIARTPSV---NIGCCIENVLLQQNLTVG 229
                                                                                                                                                          ILQQTLT---ELSVIANFSEPEIKLAQNVTGNSGINLTCTSKQGHPKPKKMYFLITNSTN 183
                                                                                                                                                                                                                                      EHYLGTEKLDSVNAKYLGRTSFD-----RNNWTLRLHNVQIKDMGSYDCFIQKKPPTGSI 126
                                                                                                                                                                                                                                                                         YHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQ----SL 120
                                                                                                                                                                                                                                                                                                                  GLAILIFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWQ-DQQKLVLY 71
SKPLNFTQE----FPSPQTYWKEITASVTVALLLVMLLII-----
                                                                          EYGDNMQISQD------NVTELFSISNSLSLSFPDGVWHMTVVCVLET----ESMKIS
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Borriello, Francescopaolo
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(617)227-5941
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                              12.2%; Score 182; DB 4; Length 314; 23.6%; Pred. No. 3.1e-10; tive 61; Mismatches 117; Indels 48;
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RESULT 10
US-08-724-394A-1
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PCT-US95-02576-13
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APPLICANT:
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Best Local Similarity
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: US 08/205
APPLICATION UMBER: US 08/205
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: MANDITON NUMBER: 36,207
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)227-594: INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
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CITY: Boston
STATE: Massac
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                                                                                                                                                                                                                                                                                                                                                                             13 GLAILIFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWQ-DQQKLVLY 71
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                                                                           SKPLNETQE----FPSPQTYWKEITASVTVALLLVMLLII-----VCHKKPNQPS
                                                                                                                                                   EYGDNMQISQD-----NVTELFSISNSLSLSFPDGVWHMTVVCVLET----ESMKIS
                                                                                                                                                                                    ---DNSLLDQALQNDTVFLNMRGLYDVVSVLRIARTPSV---NIGCCIENVLLQQNLTVG
                                                                                                                                                                                                                           ILQQTLT---ELSVIANFSEPEIKLAQNVTGNSGINLTCTSKQGHPKPKKMYFLITNSTN 183
                                                                                                              SQTGNDIGERDKITENPVSTGEKNAATWSILAVLCLLVVVAVAIGWVCRDRCLQHS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                         70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (617)227-7400
(617)227-5941
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23.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 182; DB 5;
Pred. No. 3.1e-10;
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Sequence 1, Application US/08724394A Patent No. 5872237

GENERAL INFORMATION: APPLICANT: Feder,

John

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Sequence 2, Application PC/TUS9409642
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FOO amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/724
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FILLS, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 58'
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thomas, Winston APPLICANT: Tsuchihashi, Zer
                                                                                              256 XXXXXXXXXXXXXILMVLGLLTIGSIFFTW
                                                                                                                                                                        210 IIRDTSTKNVSCYIONLLI
                                                                                                                                                                                                                                            154 SM-QVQENGEICLECTSVGWYPEPQVQWRTSKGEKFPSTSESRNP---DEEGLFTVAASV 209
                                                                                                                                                                                                         204 RIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGERDKITENPVSTGEKNAATW-----
                                                                                                                                                                                                                                                                              144 SAPHSPSQDELTFTCTSINGYPRPNYYWINKTDNSLLDQALQNDTVFLNMRGLYDVVSVL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 589 amino
TYPE: amino acid
STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                                                      84 ALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQSLGFQEVLSVEVTLHVAANFSVPVV 143
                                                                                                                                                                                                                                                                                                                                                                                                                              25 VRAMVGSDVELSC-ACPEGSRFDLNDVYVYWQTSESKTVVTYHIPQNSSLENVDSRYRNR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Region LOCATION: 1.589 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             41 ILAVVGEDAELPCRLSPNASAEHLE----LRWFRKKVSPAVLVHRDGREQEAEQMPEYRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                   -----SILAVLCLLVVVAVAIGW 275
                                                                                                                                                                                                                                                                                                                     ATLVQDGIAKGRVALRIRGVRVSDDGEYTCF-FREDGSYEEAL---VHLKVAALGSDPHI 153
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Ruddy, David A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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Peter M.
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23.7%;
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Pred. No. 6.2e-09;
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RESULT 12
US-08-456-104-2
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Sequence 2, Application Patent No. 5861310 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08
FILING DATE: 13-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Purified Mammalian CTLA-4 HITITLE OF INVENTION: Protein and Related Reagents NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation, M-3-W STREET: One Giralda Farms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: System Software 7.1 SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                  114 MIRIHOMNSELSVLANFSOPEIVPISNITENVYINLTCSSIHGYPEPKKMSVLLRTKNST 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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OPERATING SYSTEM: System Softw
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                                                                                                                                                          TGNDIGERDKITENPVSTGEKNA-----ATWSILAVL-----CLLVVVAVAIGWVCRDR 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESKTV 62
                                                                                                                                                                                                IEYDGIMQKSQD----
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                                                                                                                         DKTRLLSSPFSIELEDPQPPPDHIPW-ITAVLPTVIICVMVFCLILWKWKKKKR 269
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                                      US/08456104
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21.7%; Pred. No. 1.4
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Mismatches
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nes 121;
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APPLICANT:

Freeman,

Gordon J.

APPLICANT:

Nadler,

Lee

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                                   ; Sequence 2, Application
; Patent No. 5942607
; GENERAL INFORMATION:
APPLICANT: Freeman,
                                                                                                                 RESULT 13
US-08-101-624-2
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TELEFAX: (617) 227-59
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: RP TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNETY/AGENT INFORMATION:
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   APPLICANT:
                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     122
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APPLICATION NUMBER: 08/1
FILING DATE: 26-JUL-1993
                                                                                                                                                                                            223
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                                                                                                                                                                                                                              232 TGNDIGERDKITENPVSTGEKNA-----ATWSILAVL-----CLLVVVAVAIGWVCRDR 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 VTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLV-LSQSLG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                         NEVYLGK-EKFDSVHSKYMGRTSFD-----SDSWTLRLHNLQIKDKGLYQCIIHHKKPTG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGLSNILFVM-AFILISGAAPIKIQAYFNETADIPCQFANSQNQSISELVVFWQDQENIVL 65
                                                                                                                                                                                                                                                                                                       LD-----QALQNDTVFLNMRGLYDVVSVLRIA---RTPSVNIGCCIENVLLQQNLTVGSQ 231
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                                                                                             Application US/08101624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 amino acids
Freeman, Gordon J. Nadler, Lee M. Gray, Gary S.
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21.7%; Pred. No. 1.
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222

NUMBER OF SEQUENCES:

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; MOLECULE TYPE: protein US-08-101-624-2
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US-08-479-744A-2
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                                                                                                                         Sequence 2, Applic Patent No. 6084067
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GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands
TITLE OF INVENTION: Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acid
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: LAHIVE & COCKFIELD
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            232
                                                                                                                                                                                                                                                   223 -----DKTRLLSSPFSIELEDPQPPPDHIPW-ITAVLPTVIICVMVFCLILWKWKKKKR
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Local Similarity 21.7%;
nes 65; Conservative 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 26-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mandragouras, Amy E REGISTRATION NUMBER: 36,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 MGLSNILFVM-AFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENLVL 65
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                                                                                                                                                                                                                                                                                         TGNDIGERDKITENPVSTGEKNA-----ATWSILAVL-----CLLVVVAVAIGWVCRDR
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Pred. No. 1.5e-08;
1; Mismatches 121;
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                                                       Sequence 2, Application US/08280757B Patent No. 6130316 GENERAL INFORMATION:
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                                        APPLICANT:
 MPPLICANT:
                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: RP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
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ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 60 State Street
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                                                                                                                                                                                                                                                                                                                                                                     122 FQEVLSVEVTLHVAANFSVP-VVSAPHSPSQDELTFTCTSINGYPRP-NVYWINKTDNSL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/2 FILING DATE: 26-JUL-1994 APPLICATION NUMBER: 08/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/479,744A FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESKTV 62
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                                                                                                                                                                                     -----DKTRLLSSPFSIELEDPQPPPDHIPW-ITAVLPTVIICVMVFCLILWKWKKKKR
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Gray, Gary S.
                   Nadler, Lee M.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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3-NOV-1993
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26-JULY-1993
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21.7%;
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Pred. No. 1.5e-08;
1; Mismatches 121;
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INFORMATION FOR SEQ
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Uses Therefor TITLE OF INVENTION: Uses Therefor TITLE OF THORNGES: 53
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                        232 TGNDIGERDKITENPVSTGEKNA-----ATWSILAVL-----CLLVVVAVAIGWVCRDR
                                                                                                                                                                                                                     120 MIRIHQMNSELSVLANFSQPEIVPISNITENVYINLTCSSIHGYPEPKKMSVLLRTKNST 179
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FILING DATE: 19-AUG-1
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                                                                    -----DKTRLLSSPFSIELEDPQPPPDHIPW-ITAVLPTVIICVMVFCLILWKWKKKKR
                                                                                                                                            IEYDGIMQKSQD--
                                                                                                                                                                                                                                                                                         NEVYLGK-EKFDSVHSKYMGRTSFD-----SDSWTLRLHNLQIKDKGLYQCIIHHKKPTG
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amino acid
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227-5941
207: 2:
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21.7%; Pred. No. 1.
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IntelliGenetics

GENALIGN -Release 5.4

5.4

Multiple Sequence Alignment Program

Solution Parameters:

Wed 23 Oct 102 14:25:42-PDT

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        US-09-728-18
        1 MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYVYWQTSESKT

        US-09-728-16
        1 MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYYVWQTSESKT

        US-09-728-16
        1 MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDVYYVWQTSESKT

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 US-09-728-
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14. US-09-728-420C-18
9. US-09-728-420C-12
10. US-09-728-420C-13
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DELetion-weight
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                 QEVLSVEVTLHVAANFSVPVVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTDNSLLDQA
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US-09-728-US-09-728us-09-728-**3** US-09-728-US-09-728-224 NPVSTGEKNAATWSILAVLCLLVVVAVAIGWVCRDRCLQHSYAG 163 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGERDKITE NPVSTGEKNAATWSILAVLCLLVVVAVAIGWVCRDRCLQHSYAGawavspeteltghv LQNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDIGERDKITE

Alignment score -612.00

Scoring matrix:

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